<110> Mercken, Marc; Benson, Jacqueline M.

<120> ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES

<130> CEN5021 NP

<140> US 10/810,881
<141> 2004-03-26

<150> US 60/458,474
<151> 2003-03-28

<150> US 60/458,469
<151> 2003-03-28

<150> US 60/458,509
<151> 2003-03-28

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<151> 2003-03-28

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Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Xaa
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Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Xaa Arg
35 40 45

Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu
50 55 60

Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
65 70 75 80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Gly
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Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
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Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
115 120 125

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Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Xaa Trp
            20                  25                  30

Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Xaa Arg Leu
        35                  40                  45

Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Met Thr
    50                  55                  60

Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Xaa Trp
65                  70                  75                  80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Pro Thr Ser Pro
                85                  90                  95

Lys Val Phe Pro Leu Ser Leu Ser Ser Lys Ser Thr Ser Gly Gly Thr
            100                 105                 110

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
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Glu Val Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
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Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Xaa
            20                  25                  30

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Xaa Arg
        35                  40                  45

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
    50                  55                  60

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
65                  70                  75                  80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Ala
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Pro Ser Val Phe
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Xaa Trp
            20                  25                  30

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Xaa Arg Phe
        35                  40                  45

Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
    50                  55                  60

Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Thr Xaa Trp
65                  70                  75                  80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
                85                  90                  95
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Ser Val Phe Pro Leu Ala
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Gly Xaa Trp
20 25 30

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Xaa Arg Phe
35 40 45

Thr Ile Ser Arg Asp Asp Ser Lys Ser Ile Ala Tyr Leu Gln Met Asn
50 55 60

Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg Asn Xaa
65 70 75 80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Thr Lys Gly
85 90 95

Pro Ser Val Leu Pro
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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ser Ile Ser Ser

20 25 30

Ser Xaa Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
35 40 45

Xaa Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
50 55 60

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
65 70 75 80

Arg Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Pro Thr
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Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys
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Glu Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
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Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Xaa
            20                  25                  30

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Xaa Gln
        35                  40                  45

Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln Trp
    50                  55                  60

Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Xaa
65                  70                  75                  80

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Ala
                85                  90                  95

Pro Ser Val Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
            100                 105                 110

Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
        115                 120                 125

Ile Thr Phe Ser
    130
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Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
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Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Xaa Trp
            20                  25                  30

Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu Gly Xaa Arg Ile
        35                  40                  45

Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln Leu Asn
    50                  55                  60

Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa Trp
65                  70                  75                  80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala Pro
                85                  90                  95

Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr Ser
            100                 105                 110

Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro
        115                 120                 125
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Xaa Trp
            20                  25                  30

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Xaa Arg Phe
        35                  40                  45

Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser
    50                  55                  60

Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa Trp
65                  70                  75                  80

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ser
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Asp Arg Arg Val Thr Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly
            20                  25                  30

Lys Ala Pro Lys Leu Leu Ile Tyr Xaa Gly Val Pro Ser Arg Phe Ser
        35                  40                  45

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
    50                  55                  60

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Xaa Phe Gly Gln Gly Thr Lys
65                  70                  75                  80

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
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Gln Pro Ala Ser Ile Ser Cys Xaa Trp Tyr Leu Gln Lys Pro Gly Gln
            20                  25                  30

Ser Pro Gln Leu Leu Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly
        35                  40                  45

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
    50                  55                  60

Glu Asp Val Gly Val Tyr Tyr Cys Xaa Phe Gly Gln Gly Thr Lys Val
65                  70                  75                  80

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
                85                  90
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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln
            20                  25                  30

Ala Pro Arg Leu Leu Ile Tyr Xaa Gly Ile Pro Asp Arg Phe Ser Gly
        35                  40                  45

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
    50                  55                  60

Glu Asp Phe Ala Val Tyr Tyr Cys Xaa Phe Gly Gln Gly Thr Lys Val
65                  70                  75                  80
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Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
85 90

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Asp Lys Val Asn Ile Ser Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Glu
20 25 30

Ala Ala Ile Phe Ile Ile Gln Xaa Gly Ile Pro Pro Arg Phe Ser Gly
35 40 45

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Glu Ser

50 55 60

Glu Asp Ala Ala Tyr Tyr Phe Cys Xaa Leu Arg His Phe Trp Pro Gly
65 70 75 80

Asp Gln Ala Ala Gly
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Glu Ile Val Met Thr Gln Ser Pro Val Asn Leu Ser Met Ser Ala Gly
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Glu Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Phe Ile
20 25 30

Tyr Xaa Gly Ile Ser Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
35 40 45

Phe Thr Leu Thr Ile Thr Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr
50 55 60

Tyr Cys Xaa Phe Gly Gln Gly Thr Lys Leu Asp Ile Lys Arg Thr
65 70 75

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<400> 15

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Xaa
1 5 10 15

Trp Tyr Gln His Lys Pro Gly Gln Ala Pro Arg Leu Val Ile His Xaa
20 25 30

Gly Ile Ser Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
35 40 45

Leu Thr Ile Thr Arg Leu Glu Pro Glu Asp Phe Ala Leu Tyr Tyr Cys
50 55 60

Xaa Phe Gly Gln Gly Thr Lys Leu Asp Phe Lys Arg Thr
65 70 75

<210> 16
<211> 98
<212> PRT
<213> Homo sapiens

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<223> framework 2

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<223> framework 3

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<223> complementarity determinng region 3 (CDR3). X is any amino acid.

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<223> framework 4

<400> 16

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Xaa Trp Tyr Gln Gln Leu Pro Gly Thr Ala
20 25 30

Pro Lys Leu Leu Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
35 40 45

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
50 55 60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65 70 75 80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
85 90 95

Ser Ser

<210> 17
<211> 99
<212> PRT
<213> Homo sapiens

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<223> Lambda1b light chain variable region

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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> framework 2

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<223> framework 3

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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<223> framework 4

<400> 17

Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly
1 5 10 15

Gln Lys Val Thr Ile Ser Cys Xaa Trp Tyr Gln Gln Leu Pro Gly Thr
20 25 30

Ala Pro Lys Leu Leu Ile Tyr Xaa Gly Ile Pro Asp Arg Phe Ser Gly
35 40 45

Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln Thr
50 55 60

Gly Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu
65 70 75 80

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
85 90 95

Pro Ser Ser

<210> 18
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<212> PRT
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<223> framework 1

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<223> framework 2

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<223> framework 4

<400> 18

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Xaa Trp Tyr Gln Gln His Pro Gly Lys Ala
20 25 30

Pro Lys Leu Met Ile Tyr Xaa Gly Val Ser Asn Arg Phe Ser Gly Ser
35 40 45

Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala Glu
50 55 60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Thr Lys Leu
65 70 75 80

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
85 90 95

Pro Ser Ser

<210> 19
<211> 107
<212> PRT
<213> Homo sapiens

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<223> Lambda3a light chain variable region

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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> framework 2vv

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<223> framework 3

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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<223> framework 4

<400> 19

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Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                  10                  15

Thr Ala Arg Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            20                  25                  30

Pro Val Leu Val Ile Tyr Xaa Gly Ile Pro Glu Arg Phe Ser Gly Ser
        35                  40                  45

Ser Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
    50                  55                  60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65                  70                  75                  80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
                85                  90                  95

Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr
            100                 105
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<210> 20
<211> 93
<212> PRT
<213> Homo sapiens

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<223> Lambda3b light chain variable region

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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> framework 2

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<222> (41)..(72)
<223> framework 3

<220>
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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (74)..(93)
<223> framework 4

<400> 20

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala
20 25 30

Pro Val Leu Val Val Tyr Asp Xaa Gly Ile Pro Glu Arg Phe Ser Gly
35 40 45

Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala
50 55 60

Gly Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu
65 70 75 80

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Thr Val Thr
85 90

<210> 21
<211> 98
<212> PRT
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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> framework 2

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<223> framework 3

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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<223> framework 4

<400> 21

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Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1               5                   10                  15

Thr Ala Ser Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ser
            20                  25                  30

Pro Val Leu Val Ile Tyr Xaa Gly Ile Pro Glu Arg Phe Ser Gly Ser
        35                  40                  45

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
    50                  55                  60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65                  70                  75                  80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Arg Ser Leu Cys Pro Pro
                85                  90                  95

Pro Pro
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<210> 22
<211> 98
<212> PRT
<213> Homo sapiens

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<223> Lambda3e light chain variable region

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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> framework 2

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<223> framework 3

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<220>
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<223> framework 4

<400> 22

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Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1               5                  10                  15

Thr Val Arg Ile Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Gln Ala
            20                  25                  30

Pro Val Leu Val Ile Tyr Xaa Gly Ile Pro Asp Arg Phe Ser Gly Ser
        35                  40                  45

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
    50                  55                  60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65                  70                  75                  80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
                85                  90                  95
```

Ser Ser

<210> 23
<211> 94
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<213> Homo sapiens

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<223> Lambda4a light chain variable region

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<223> framework 1

<220>
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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

<220>
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<223> framework 2

<220>
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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<223> framework 3

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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<223> framework 4

<400> 23

Gln Pro Val Leu Thr Gln Ser Ser Ser Ala Ser Ala Ser Leu Gly Ser
1 5 10 15

Ser Val Lys Leu Thr Cys Xaa Trp His Gln Gln Gln Pro Gly Lys Ala
20 25 30

Pro Arg Tyr Leu Met Lys Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
35 40 45

Ser Ser Gly Ala Asp Arg Tyr Leu Thr Ile Ser Asn Leu Gln Ser Glu
50 55 60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65 70 75 80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
85 90

<210> 24
<211> 95
<212> PRT
<213> Homo sapiens

<220>
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<223> framework 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

<220>
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<223> framework 2

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<223> framework 3

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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<222> (73)..(95)
<223> framework 4

<400> 24

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15

Ser Val Lys Leu Thr Cys Xaa Trp His Gln Gln Gln Pro Glu Lys Gly
20 25 30

Pro Arg Tyr Leu Met Lys Xaa Gly Ile Pro Asp Arg Phe Ser Gly Ser

35 40 45

Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser Ser Leu Gln Ser Glu
50 55 60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Ile Gly Gly Gly Thr
65 70 75 80

Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Ser
85 90 95

<210> 25
<211> 88
<212> PRT
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<223> Lambda5 light chain variable region

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<223> framework 1

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<223> framework 2

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<223> framework 3

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<222> (75)..(75)
<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<222> (76)..(88)
<223> framework 4

<400> 25

Gln Ala Val Leu Thr Gln Pro Ser Ser Leu Ser Ala Ser Pro Gly Ala
1 5 10 15

Ser Ala Ser Leu Thr Cys Xaa Trp Tyr Gln Gln Lys Pro Gly Ser Pro
20 25 30

Pro Gln Tyr Leu Leu Arg Tyr Xaa Gly Val Pro Ser Arg Phe Ser Gly
35 40 45

Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile Leu Leu Ile Ser Gly Leu
50 55 60

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr
65 70 75 80

Lys Leu Thr Val Leu Ser Gln Pro
85

<210> 26
<211> 101
<212> PRT
<213> Homo sapiens

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<223> Lambda6 light chain variable region

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<223> framewrok 1

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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

<220>
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<223> framewrok 3

<220>
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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

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<222> (75)..(101)
<223> framewrok 4

<400> 26

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Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1               5                   10                  15

Thr Val Thr Ile Ser Cys Xaa Trp Tyr Gln Gln Arg Pro Gly Ser Ala
            20                  25                  30

Pro Thr Thr Val Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
        35                  40                  45

Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly Leu Lys
    50                  55                  60

Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys
65                  70                  75                  80

Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
                85                  90                  95

Pro Pro Ser Ser Ser
            100
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<210> 27
<211> 89
<212> PRT
<213> Homo sapiens

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<223> Lambda7 light chain variable region

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<222> (1)..(22)
<223> framework 1

<220>
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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

<220>
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<222> (24)..(38)
<223> framework 2

<220>
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<222> (39)..(39)
<223> complementarity determinng region 2 (CDR2), X is any amino acid.

<220>
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<222> (40)..(71)
<223> framework 3

<220>
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<222> (72)..(72)
<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (73)..(89)
<223> framework 4

<400> 27

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Xaa Trp Phe Gln Gln Lys Pro Gly Gln Ala
20 25 30

Pro Arg Ala Leu Ile Tyr Xaa Trp Thr Pro Ala Arg Phe Ser Gly Ser
35 40 45

Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu
50 55 60

Asp Glu Ala Glu Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65 70 75 80

Val Leu Gly Gln Pro Lys Ala Ala Pro
85

<210> 28
<211> 89
<212> PRT
<213> Homo sapiens

<220>
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<223> Lambda8 light chain variable region

<220>
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<223> framework 1

<220>
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<223> complementarity determinng region 1 (CDR1), X is 5-25 (14) of any amino acid.

<220>
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<222> (24)..(38)
<223> framework 2

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> complementarity determinng region 2 (CDR2), X is any amino acid.

<220>

<221> MISC_FEATURE
<222> (40)..(71)
<223> framework 3

<220>
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<222> (72)..(72)
<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
<221> MISC_FEATURE
<222> (73)..(89)
<223> framework 4

<400> 28

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Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1               5                  10                  15

Thr Val Thr Leu Thr Cys Xaa Trp Tyr Gln Gln Thr Pro Gly Gln Ala
            20                  25                  30

Pro Arg Thr Leu Ile Tyr Xaa Gly Val Pro Asp Arg Phe Ser Gly Ser
        35                  40                  45

Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala Gln Ala Asp
    50                  55                  60

Asp Glu Ser Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65                  70                  75                  80

Val Leu Gly Gln Pro Lys Ala Ala Pro
                85
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<210> 29
<211> 91
<212> PRT
<213> Homo sapiens

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<223> Lambda9 light chain variable region

<220>
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<222> (1)..(22)
<223> framework 1

<220>
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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

<220>
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<222> (24)..(38)
<223> framework 2

<220>

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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

<220>
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<222> (40)..(79)
<223> framework 3

<220>
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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
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<222> (81)..(91)
<223> framework 4

<400> 29

Gln Pro Val Leu Thr Gln Pro Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15

Ser Val Thr Leu Thr Cys Xaa Trp Tyr Gln Gln Arg Pro Gly Lys Gly
20 25 30

Pro Arg Phe Val Met Arg Xaa Gly Ile Pro Asp Arg Phe Ser Val Leu
35 40 45

Gly Ser Gly Leu Asn Arg Tyr Leu Thr Ile Lys Asn Ile Gln Glu Glu
50 55 60

Asp Glu Ser Asp Tyr His Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65 70 75 80

Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val
85 90

<210> 30
<211> 87
<212> PRT
<213> Homo sapiens

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<223> Lambda10 light chain variable region

<220>
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<223> framework 1

<220>
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<223> complementarity determinng region 1 (CDR1), X is any amino acid.

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<223> framework 2

<220>
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<223> complementarity determinng region 2 (CDR2), X is any amino acid.

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<223> framework 3

<220>
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<223> complementarity determinng region 3 (CDR3), X is any amino acid.

<220>
<221> MISC_FEATURE
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<223> framework 4

<400> 30

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Gln Ala Gly Leu Thr Gln Pro Pro Ser Val Ser Lys Gly Leu Arg Gln
1               5                  10                  15

Thr Ala Thr Leu Thr Cys Xaa Trp Leu Gln Gln His Gln Gly His Pro
            20                  25                  30

Pro Lys Leu Leu Ser Tyr Xaa Gly Ile Ser Glu Arg Phe Ser Ala Ser
        35                  40                  45

Arg Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Leu Gln Pro Glu
    50                  55                  60

Asp Glu Ala Asp Tyr Tyr Cys Xaa Phe Gly Gly Gly Thr Lys Leu Thr
65                  70                  75                  80

Val Leu Gly Gln Pro Lys Ala
                85
```

<210> 31
<211> 354
<212> PRT
<213> Homo sapiens

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<223> IgA1 heavy chain constant region

<220>
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<223> CH1

<220>

<221> MISC_FEATURE
<222> (103)..(121)
<223> hinge

<220>
<221> MISC_FEATURE
<222> (122)..(222)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (223)..(354)
<223> CH3

<400> 31

```
Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
1               5                  10                  15

Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
            20                  25                  30

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
        35                  40                  45

Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
    50                  55                  60

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
65                  70                  75                  80

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
                85                  90                  95

Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
            100                 105                 110

Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
        115                 120                 125

Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
    130                 135                 140

Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
145                 150                 155                 160

Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
                165                 170                 175

Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
            180                 185                 190

Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
        195                 200                 205
```

```
Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
    210                 215                 220

Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glx Glu Glu
225                 230                 235                 240

Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe
                245                 250                 255

Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu
            260                 265                 270

Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln
        275                 280                 285

Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu
    290                 295                 300

Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala
305                 310                 315                 320

Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys
                325                 330                 335

Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr
            340                 345                 350

Cys Tyr
```

<210> 32
<211> 340
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(340)
<223> IgA2 heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(102)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (103)..(108)
<223> hinge

<220>
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<222> (109)..(209)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (210)..(340)
<223> CH3

<400> 32

```
Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp Ser Thr
1               5                  10                  15

Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly Phe Phe
            20                  25                  30

Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Asn Val
        35                  40                  45

Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
    50                  55                  60

Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro Asp Gly
65                  70                  75                  80

Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
                85                  90                  95

Val Thr Val Pro Cys Pro Val Pro Pro Pro Pro Pro Cys Cys His Pro
            100                 105                 110

Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser
        115                 120                 125

Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly
    130                 135                 140

Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly
145                 150                 155                 160

Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu
                165                 170                 175

Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr Cys Thr
            180                 185                 190

Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile Thr Lys
        195                 200                 205

Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser
    210                 215                 220

Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg
225                 230                 235                 240
```

```
Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln
                245                 250                 255

Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro
            260                 265                 270

Ser Gln Gly Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala
        275                 280                 285

Ala Glu Asp Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His
    290                 295                 300

Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala
305                 310                 315                 320

Gly Lys Pro Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp
                325                 330                 335

Gly Thr Cys Tyr
            340
```

<210> 33
<211> 384
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(384)
<223> IgD heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(101)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (102)..(135)
<223> hinge 1

<220>
<221> MISC_FEATURE
<222> (136)..(159)
<223> hinge 2

<220>
<221> MISC_FEATURE
<222> (160)..(267)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (268)..(384)
<223> CH3

<400> 33

```
Ala Pro Thr Lys Ala Pro Asp Val Phe Pro Ile Ile Ser Gly Cys Arg
```

```
1               5                   10                  15

His Pro Lys Asp Asn Ser Pro Val Val Leu Ala Cys Leu Ile Thr Gly
            20                  25                  30

Tyr His Pro Thr Ser Val Thr Val Thr Trp Tyr Met Gly Thr Gln Ser
        35                  40                  45

Gln Pro Gln Arg Thr Phe Pro Glu Ile Gln Arg Arg Asp Ser Tyr Tyr
    50                  55                  60

Met Thr Ser Ser Gln Leu Ser Thr Pro Leu Gln Gln Trp Arg Gln Gly
65                  70                  75                  80

Glu Tyr Lys Cys Val Val Gln His Thr Ala Ser Lys Ser Lys Lys Glu
                85                  90                  95

Ile Phe Arg Trp Pro Glu Ser Pro Lys Ala Gln Ala Ser Ser Val Pro
            100                 105                 110

Thr Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala
        115                 120                 125

Pro Ala Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys
    130                 135                 140

Glu Lys Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu
145                 150                 155                 160

Cys Pro Ser His Thr Gln Pro Leu Gly Val Tyr Leu Leu Thr Pro Ala
                165                 170                 175

Val Gln Asp Leu Trp Leu Arg Asp Lys Ala Thr Phe Thr Cys Phe Val
            180                 185                 190

Val Gly Ser Asp Leu Lys Asp Ala His Leu Thr Trp Glu Val Ala Gly
        195                 200                 205

Lys Val Pro Thr Gly Gly Val Glu Glu Gly Leu Leu Glu Arg His Ser
    210                 215                 220

Asn Gly Ser Gln Ser Gln His Ser Arg Leu Thr Leu Pro Arg Ser Leu
225                 230                 235                 240

Trp Asn Ala Gly Thr Ser Val Thr Cys Thr Leu Asn His Pro Ser Leu
                245                 250                 255

Pro Pro Gln Arg Leu Met Ala Leu Arg Glu Pro Ala Ala Gln Ala Pro
            260                 265                 270
```

Val Lys Leu Ser Leu Asn Leu Leu Ala Ser Ser Asp Pro Pro Glu Ala
275 280 285

Ala Ser Trp Leu Leu Cys Glu Val Ser Gly Phe Ser Pro Pro Asn Ile
290 295 300

Leu Leu Met Trp Leu Glu Asp Gln Arg Glu Val Asn Thr Ser Gly Phe
305 310 315 320

Ala Pro Ala Arg Pro Pro Pro Gln Pro Arg Ser Thr Thr Phe Trp Ala
325 330 335

Trp Ser Val Leu Arg Val Pro Ala Pro Pro Ser Pro Gln Pro Ala Thr
340 345 350

Tyr Thr Cys Val Val Ser His Glu Asp Ser Arg Thr Leu Leu Asn Ala
355 360 365

Ser Arg Ser Leu Glu Val Ser Tyr Val Thr Asp His Gly Pro Met Lys
370 375 380

<210> 34
<211> 497
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(497)
<223> IgE heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(103)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (104)..(210)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (211)..(318)
<223> CH3

<220>
<221> MISC_FEATURE
<222> (319)..(497)
<223> CH4

<400> 34

Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys Cys Lys
1 5 10 15

Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu Ala Thr
20 25 30

```
Gly Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly Ser Leu
        35                  40                  45

Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu Ser Gly
    50                  55                  60

His Tyr Ala Thr Ile Ser Leu Leu Thr Val Ser Gly Ala Trp Ala Lys
65                  70                  75                  80

Gln Met Phe Thr Cys Arg Val Ala His Thr Pro Ser Ser Thr Asp Trp
                85                  90                  95

Val Asp Asn Lys Thr Phe Ser Val Cys Ser Arg Asp Phe Thr Pro Pro
            100                 105                 110

Thr Val Lys Ile Leu Gln Ser Ser Cys Asp Gly Gly Gly His Phe Pro
        115                 120                 125

Pro Thr Ile Gln Leu Leu Cys Leu Val Ser Gly Tyr Thr Pro Gly Thr
    130                 135                 140

Ile Asn Ile Thr Trp Leu Glu Asp Gly Gln Val Met Asp Val Asp Leu
145                 150                 155                 160

Ser Thr Ala Ser Thr Thr Gln Glu Gly Glu Leu Ala Ser Thr Gln Ser
                165                 170                 175

Glu Leu Thr Leu Ser Gln Lys His Trp Leu Ser Asp Arg Thr Tyr Thr
            180                 185                 190

Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr Lys Lys
        195                 200                 205

Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro
    210                 215                 220

Ser Pro Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu
225                 230                 235                 240

Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser
                245                 250                 255

Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys
            260                 265                 270

Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr
        275                 280                 285

Arg Asp Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro
```

290 295 300

His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser Gly Pro
305 310 315 320

Val Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu
325 330 335

Trp Pro Gly Ser Arg Asp Lys Arg Thr Leu Ala Cys Leu Ile Gln Asn
340 345 350

Phe Met Pro Glu Asp Ile Ser Val Gln Trp Leu His Asn Glu Val Gln
355 360 365

Leu Pro Asp Ala Arg His Ser Thr Thr Gln Pro Arg Lys Thr Lys Gly
370 375 380

Ser Gly Phe Phe Val Phe Ser Arg Leu Glu Val Thr Arg Ala Glu Trp
385 390 395 400

Glu Gln Lys Asp Glu Phe Ile Cys Arg Ala Val His Glu Ala Ala Ser
405 410 415

Pro Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys Asp
420 425 430

Val Cys Val Glu Glu Ala Glu Gly Glu Ala Pro Trp Thr Trp Thr Gly
435 440 445

Leu Cys Ile Phe Ala Ala Leu Phe Leu Leu Ser Val Ser Tyr Ser Ala
450 455 460

Ala Leu Thr Leu Leu Met Val Gln Arg Phe Leu Ser Ala Thr Arg Gln
465 470 475 480

Gly Arg Pro Gln Thr Ser Leu Asp Tyr Thr Asn Val Leu Gln Pro His
485 490 495

Ala

<210> 35
<211> 339
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(339)
<223> IgG1 heavy chain constant region

<220>

<221> MISC_FEATURE
<222> (1)..(98)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (99)..(113)
<223> hinge

<220>
<221> MISC_FEATURE
<222> (114)..(223)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (224)..(339)
<223> CH3

<400> 35

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                  10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
        115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190
```

```
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asx Asn Gly Gln Pro Glu
            260                 265                 270

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
        275                 280                 285

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
    290                 295                 300

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
305                 310                 315                 320

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr His Thr Cys Pro
                325                 330                 335

Pro Cys Pro
```

<210> 36
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(326)
<223> IgG2 heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(98)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (99)..(110)
<223> hinge

<220>
<221> MISC_FEATURE
<222> (111)..(219)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (220)..(326)
<223> CH3

<400> 36

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                  10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240
```

```
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    290                 295                 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305                 310                 315                 320

Ser Leu Ser Pro Gly Lys
                325
```

<210> 37
<211> 377
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(377)
<223> IgG3 heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(98)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (99)..(115)
<223> hinge 1

<220>
<221> MISC_FEATURE
<222> (116)..(130)
<223> hinge 2

<220>
<221> MISC_FEATURE
<222> (131)..(145)
<223> hinge 3

<220>
<221> MISC_FEATURE
<222> (146)..(160)
<223> hinge 4

<220>
<221> MISC_FEATURE
<222> (161)..(270)
<223> CH2

<220>

<221> MISC_FEATURE
<222> (271)..(377)
<223> CH3

<400> 37

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                  10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
            100                 105                 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
        115                 120                 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
    130                 135                 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145                 150                 155                 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
                165                 170                 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            180                 185                 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
        195                 200                 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
    210                 215                 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225                 230                 235                 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
```

245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 38
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(327)
<223> IgG4 heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(98)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (99)..(110)
<223> hinge

<220>
<221> MISC_FEATURE
<222> (111)..(220)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (221)..(327)
<223> CH3

<400> 38

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1               5                  10                  15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
            100                 105                 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
        115                 120                 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
    130                 135                 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145                 150                 155                 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
                165                 170                 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            180                 185                 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
        195                 200                 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
    210                 215                 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225                 230                 235                 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                245                 250                 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
            260                 265                 270
```

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325

<210> 39
<211> 476
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(476)
<223> IgM heavy chain constant region

<220>
<221> MISC_FEATURE
<222> (1)..(104)
<223> CH1

<220>
<221> MISC_FEATURE
<222> (105)..(217)
<223> CH2

<220>
<221> MISC_FEATURE
<222> (218)..(323)
<223> CH3

<220>
<221> MISC_FEATURE
<222> (324)..(476)
<223> CH4

<400> 39

Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
1 5 10 15

Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
20 25 30

Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser
35 40 45

Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
50 55 60

```
Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
65                  70                  75                  80

Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
                85                  90                  95

Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys
            100                 105                 110

Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
        115                 120                 125

Ser Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln
    130                 135                 140

Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val
145                 150                 155                 160

Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr
                165                 170                 175

Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser
            180                 185                 190

Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln
        195                 200                 205

Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg
    210                 215                 220

Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
225                 230                 235                 240

Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
                245                 250                 255

Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
            260                 265                 270

Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
        275                 280                 285

Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
    290                 295                 300

Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
305                 310                 315                 320

Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro
                325                 330                 335
```

```
Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys
            340                 345                 350

Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Gln Met
        355                 360                 365

Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro
    370                 375                 380

Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu
385                 390                 395                 400

Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val
                405                 410                 415

Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp
            420                 425                 430

Lys Ser Thr Gly Lys Pro Thr Ser Ala Asp Glu Glu Gly Phe Glu Asn
        435                 440                 445

Leu Trp Ala Thr Ala Ser Thr Phe Ile Val Leu Tyr Asn Val Ser Leu
    450                 455                 460

Val Met Ser Asp Thr Ala Gly Thr Cys Tyr Val Lys
465                 470                 475
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<210> 40
<211> 107
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<213> Homo sapiens

<220>
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<222> (1)..(107)
<223> Light chain kappa constant region (IgKc)

<400> 40

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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
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65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 41
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(107)
<223> Light chain lambda constant region (IgLambda)

<400> 41

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
1 5 10 15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
20 25 30

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
35 40 45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg Lys Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr
85 90 95

Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
100 105

<210> 42
<211> 5
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<220>
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<223> heavy chain (HC) complementary determining region (CDR) 1

<400> 42

Asp His Tyr Val His
1 5

<210> 43
<211> 17
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<220>
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<222> (1)..(17)
<223> HC CDR 2

<400> 43

Trp Ile Ala Pro Lys Asn Gly Tyr Ser Glu Ser Ala Pro Lys Phe Gln
1 5 10 15

Gly

<210> 44
<211> 8
<212> PRT
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<220>
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<222> (1)..(8)
<223> HC CDR 3

<400> 44

Gly Phe Tyr Asp Ser Ser Leu Tyr
1 5

<210> 45
<211> 16
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<220>
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<222> (1)..(16)
<223> light chain (LC) complementary determining region (CDR) 1

<400> 45

Lys Ser Gly Gln Ser Leu Leu Ala Arg Asp Gly Lys Thr Tyr Leu Ser
1 5 10 15

<210> 46
<211> 7
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(7)
<223> LC CDR 2

<400> 46

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 47
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(9)
<223> LC CDR 3

<400> 47

Trp Gln Gly Thr His Phe Pro Arg Thr
1 5

<210> 48
<211> 136
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(19)
<223> Signal Peptide

<220>
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<222> (20)..(49)
<223> Framework region (FR) 1

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<222> (50)..(54)
<223> CDR 1

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<222> (55)..(68)
<223> FR 2

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<223> CDR 2

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<222> (86)..(117)
<223> FR 3

<220>
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<222> (118)..(125)
<223> CDR 3

<220>
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<222> (126)..(136)
<223> FR4/J region

<400> 48

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Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Ile Gly
1               5                  10                  15

Ile Asn Ser Glu Gly Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
            20                  25                  30

Ser Gly Ala Ser Leu Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
        35                  40                  45

Lys Asp His Tyr Val His Trp Val Arg Gln Arg Pro Glu Gln Gly Leu
    50                  55                  60

Asp Trp Ile Gly Trp Ile Ala Pro Lys Asn Gly Tyr Ser Glu Ser Ala
65                  70                  75                  80

Pro Lys Phe Gln Gly Lys Ala Ser Met Thr Ala Asp Thr Ser Ser Asn
                85                  90                  95

Thr Val Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Phe Ala Gly Phe Tyr Asp Ser Ser Leu Tyr Trp Gly Gln
        115                 120                 125

Gly Thr Thr Leu Thr Val Ser Ser
    130                 135
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<210> 49
<211> 133
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (44)..(59)
<223> CDR1

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<222> (60)..(74)
<223> FR2

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<222> (75)..(81)
<223> CDR2

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<222> (82)..(113)
<223> FR3

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<222> (114)..(122)
<223> CDR3

<220>
<221> MISC_FEATURE
<222> (123)..(133)
<223> FR4/J region

<400> 49

Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
1 5 10 15

Glu Thr Asn Gly Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ala
20 25 30

Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Gly Gln Ser
35 40 45

Leu Leu Ala Arg Asp Gly Lys Thr Tyr Leu Ser Trp Leu Leu Gln Arg
50 55 60

Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr
100 105 110

Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Asn
115 120 125

Leu Glu Ile Lys Arg
130

<210> 50
<211> 42
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(42)

<223> Known beta amyloid sequence

<400> 50

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

<210> 51
<211> 408
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(408)
<223> C701 HC

<220>
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<220>
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<222> (58)..(147)
<223> FR1

<220>
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<222> (148)..(162)
<223> CDR1

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<222> (163)..(204)
<223> FR2

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<222> (205)..(255)
<223> CDR2

<220>
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<222> (256)..(351)
<223> FR3

<220>
<221> misc_feature
<222> (352)..(375)
<223> CDR3

<220>
<221> misc_feature
<222> (376)..(408)
<223> FR4/J Region

<400> 51

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ggtcagctgc agcagtctgg ggcagaactt gtgaggtcag gggcctcact caagttgtcc 120

tgcacagctt ctggcttcaa tattaaagac cactatgtac actgggtgag gcagaggcct 180

gaacagggcc tggactggat tggatggatt gctccgaaga atggttatag tgaatctgcc 240

ccgaaattcc agggcaaggc cagtatgact gcagacacat cctccaacac agtctacctg 300

cagctcagca gcctgacatc tgaggacact gccgtctatt actgttttgc agggttttac 360

gatagtagcc tctactgggg ccagggcacc actctcacag tctcttca 408

<210> 52
<211> 399
<212> DNA
<213> Homo sapiens

<220>
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<223> C701 LC

<220>
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<220>
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<223> FR1

<220>
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<222> (130)..(177)
<223> CDR1

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<222> (178)..(222)
<223> FR2

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<222> (223)..(243)
<223> CDR2

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<222> (244)..(339)
<223> FR3

<220>
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<222> (340)..(366)
<223> CDR3

<220>
<221> misc_feature
<222> (367)..(399)
<223> FR4/J Region

<400> 52
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gacgttgtaa tgacccagac tccactcact ttggcggtta ccattggaca accagcctcc 120

atctcttgca agtcaggtca gagcctctta gcaagagatg gaaagacata tttgagttgg 180

ttattacaga ggccaggcca gtctccaaag cgcctaatct atctggtgtc taaactggac 240

tctggagtcc ctgacaggtt ctctggcagt ggatcaggga cagatttcac actgaaaatc 300

aacagagtgg aggctgagga tttgggagtt tattattgct ggcaaggtac acattttcct 360

cggacgttcg gtggaggcac caacctggaa atcaaacgg 399

<210> 53
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> HC CDR1

<400> 53

Thr Ser Gly Met Gly Val Ser
1 5

<210> 54
<211> 16
<212> PRT
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<220>
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<222> (1)..(16)
<223> HC CDR2

<400> 54

His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 55
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(13)
<223> HC CDR3

<400> 55

Ser Ser Gly Ser Ile Val Ile Ala Thr Gly Phe Ala Tyr
1 5 10

<210> 56
<211> 16

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(16)
<223> LC CDR1

<400> 56

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 57
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> LC CDR2

<400> 57

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 58
<211> 9
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(9)
<223> LC CDR3

<400> 58

Phe Gln Gly Ser Arg Val Pro Leu Thr
1 5

<210> 59
<211> 142
<212> PRT
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<222> (1)..(142)
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<222> (20)..(49)

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<222> (57)..(70)
<223> FR2

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<222> (71)..(86)
<223> CDR2

<220>
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<222> (87)..(118)
<223> FR3

<220>
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<222> (119)..(131)
<223> CDR3

<220>
<221> MISC_FEATURE
<222> (132)..(142)
<223> FR4/J Region

<400> 59

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Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
1               5                  10                  15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
            20                  25                  30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
        35                  40                  45

Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
    50                  55                  60

Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
65                  70                  75                  80

Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
                85                  90                  95

Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Thr Asp Thr Ala
            100                 105                 110

Thr Tyr Tyr Cys Thr Arg Ser Ser Gly Ser Ile Val Ile Ala Thr Gly
        115                 120                 125

Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
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130 135 140

<210> 60
<211> 132
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(132)
<223> C705 LC

<220>
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<220>
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<223> FR1

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<222> (43)..(58)
<223> CDR1

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<222> (59)..(73)
<223> FR2

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<222> (74)..(80)
<223> CDR2

<220>
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<222> (81)..(112)
<223> FR3

<220>
<221> MISC_FEATURE
<222> (113)..(121)
<223> CDR3

<220>
<221> MISC_FEATURE
<222> (122)..(132)
<223> FR4/J Region

<400> 60

Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Gly
1 5 10 15

Ser Ser Ser Asp Val Met Met Thr Gln Thr Pro Leu Ser Leu Pro Val
20 25 30

Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
35 40 45

Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Met Gln Lys Pro
50 55 60

Gly Gln Ser Pro Met Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Ser Val Glu Ala Glu Asp Leu Gly Val Phe Tyr Cys
100 105 110

Phe Gln Gly Ser Arg Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
115 120 125

Glu Leu Lys Arg
130

<210> 61
<211> 426
<212> DNA
<213> Homo sapiens

<220>
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<223> C705 HC

<220>
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<220>
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<223> FR1

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<222> (148)..(168)
<223> CDR1

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<222> (169)..(210)
<223> FR2

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<222> (211)..(258)
<223> CDR2

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<222> (259)..(354)
<223> FR3

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<222> (355)..(393)

<223> CDR3

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<222> (394)..(426)
<223> FR4/J Region

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gttactctga aagagtctgg ccctgggata ttgcagccct cccagaccct cagtctgact 120

tgttctttct ctgggttttc actgagcact tctggtatgg gtgtgagctg gattcgtcag 180

ccttcaggaa agggtctgga gtggctggca cacatttact gggatgatga caaacgatat 240

aatccatccc tgaagagccg gctcacaatc tccaaggata cttccagaaa ccaggtattc 300

ctcaagatca ccagtgtgga cactacagat actgccacat actactgtac tcgaagttcc 360

ggatctattg tgattgcgac ggggtttgct tactggggcc aagggactct ggtcactgtc 420

tctgca 426

<210> 62
<211> 396
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(396)
<223> C705 LC

<220>
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<220>
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<222> (127)..(174)
<223> CDR1

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<222> (175)..(219)
<223> FR2

<220>
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<222> (220)..(240)
<223> CDR2

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<222> (241)..(336)
<223> FR3

<220>
<221> misc_feature

<222> (337)..(363)
<223> CDR3

<220>
<221> misc_feature
<222> (364)..(396)
<223> FR4/J region

<400> 62
atgaagttgc ctgttaggct gttggtgctg atgttctgga ttcctggttc cagcagtgat 60

gttatgatga cccaaactcc actctccctg cctgtcagtc ttggagatca agcctccatc 120

tcttgcagat ctagtcagag tcttgtacat agtaatggaa acacctattt agaatggtat 180

atgcagaaac caggccagtc tccaatgctc ctgatctaca aagtttccaa ccgattttct 240

ggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc 300

agcgtggagg ctgaggatct gggagttttt tactgctttc aaggttcacg tgttccgctc 360

acgttcggtg ctgggaccaa gctggagctg aaacgg 396

<210> 63
<211> 5
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(5)
<223> HC CDR1

<400> 63

Thr Ser Trp Ile Glu
1 5

<210> 64
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(17)
<223> HC CDR2

<400> 64

Glu Val Leu Pro Gly Ser Gly Lys Ser Asn His Asn Ala Asn Phe Lys
1 5 10 15

Gly

<210> 65
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> HC CDR3

<400> 65

Glu Gly Ser Asn Asn Asn Ala Leu Ala Tyr
1 5 10

<210> 66
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> LC CDR1

<400> 66

Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 67
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(7)
<223> LC CDR2

<400> 67

Asp Ser Ser Arg Leu Ala Ser
1 5

<210> 68
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(8)
<223> LC CDR3

<400> 68

Gln Asn Trp Arg Ser Ser Pro Thr
1 5

<210> 69
<211> 138
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(138)
<223> C706 HC

<220>
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<223> FR1

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<220>
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<222> (128)..(138)
<223> FR4/J Region

<400> 69

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Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1               5                  10                  15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe
        35                  40                  45

Ser Thr Ser Trp Ile Glu Trp Ile Lys Gln Arg Pro Gly His Gly Leu
    50                  55                  60

Glu Trp Ile Gly Glu Val Leu Pro Gly Ser Gly Lys Ser Asn His Asn
65                  70                  75                  80
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Ala Asn Phe Lys Gly Arg Ala Thr Phe Thr Ala Asp Thr Ala Ser Asn
                85                  90                  95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Glu Gly Ser Asn Asn Asn Ala Leu Ala Tyr Trp
        115                 120                 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ala
    130                 135
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<210> 70
<211> 128
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(128)
<223> C706 LC

<220>
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<223> FR1

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<223> CDR1

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<223> FR2

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<220>
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<222> (78)..(109)
<223> FR3

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<223> CDR3

<220>
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<222> (118)..(128)
<223> FR4/J Region

<400> 70

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1               5                  10                  15

Val Ile Ile Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
            20                  25                  30

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
        35                  40                  45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
    50                  55                  60

Pro Lys Arg Trp Ile Tyr Asp Ser Ser Arg Leu Ala Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Gly Gly Ser Gly Thr Ser Tyr Ser Pro Thr Ile
                85                  90                  95

Ser Asn Met Glu Ala Glu Asp Ala Ala Thr Tyr Phe Cys Gln Asn Trp
            100                 105                 110

Arg Ser Ser Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
        115                 120                 125
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<210> 71
<211> 414
<212> DNA
<213> Homo sapiens

<220>
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ggacatggcc ttgagtggat tggagaggtc ttacctggaa gcggtaagag taaccacaat 240

gcgaacttta agggcagggc cacatttact gcagatacag cctccaacac agcctacatg 300

cagctcagca gcctgacatc tgaggactct gccgtctatt attgtgcaag agaggggagt 360

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tctcgcttca gtggcggtgg gtctgggacc tcttactctc ccacaatcag caacatggag 300

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20 25 30

Pro Gly Ala Ser Val Lys Thr Ser Cys Lys Thr Ser Gly Tyr Ser Phe
35 40 45

Thr Glu Tyr Ile Met Ser Trp Val Arg Gln Ser His Gly Lys Ser Leu
50 55 60

Glu Trp Ile Gly Ser Ile Asn Pro Asn Thr Gly Gly Ser Arg Tyr Asn
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

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115 120 125

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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30

Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Asn
35 40 45

Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Arg
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Ser Arg Val Ser Asn Leu Ala
65 70 75 80

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser Glu Ser Gly Thr Asp Phe
85 90 95

Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Ala Gln Leu Leu Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys
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ggaaagagcc ttgagtggat tggaagtatt aatcctaaca ctggtggtag tagatacaac 240

cagaaattca agggcaaggc cacgttgact gtagataagt cctccagcac agcctacatg 300

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tatctgcaga ggccaggcca gtctcctcag ctcctgatat ctcgggtgtc caatctggcc 240

tcaggagtcc caaacaggtt cagtggcagt gagtcaggaa ctgatttcac actgagaatc 300

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